ENCLOSURE D

AMENDMENTS TO THE CLAIMS

CERTIFICATE UNDER 37 CFR 1.8(a)

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AMENDMENTS TO THE CLAIMS

The following replaces all prior listings of claims.

We claim:

1 – 28. (Cancelled)

29. (New) A labelled or unlabelled nucleic acid for the specific binding to DNA of human adenoviruses (HAdV DNA), whereby the nucleic acid comprises at least one of the following:

a) the sequence SEQ ID NO. 1 or SEQ ID NO. 3,

b) a sequence with a homology greater than 78% with respect to SEQ ID NO. 1 or SEQ ID NO. 3, or

c) a sequence that is complementary with respect to at least one sequence according to a) or b).

30. (New) A method for the detection of HAdV DNA in a sample, comprising the following steps:

- Providing a sample possibly containing HAdV DNA,
- Providing a probe that can specifically bind to the DNA of at least 35 different HAdV serotypes,
- Mixing the probe with the sample,
- Amplifying regions of DNA of each of said at least 35 HAdV serotypes actually present in the sample, so that the section to which said probe can specifically bind is amplified as well,
- Establishing conditions that allow the probe to specifically bind to sections of the amplified regions,

- Detecting the amplified DNA regions to which a probe has bound, quantitatively and/or under real-time conditions.

31. (New) A method for the detection of HAdV DNA in a sample, comprising the following steps:

- Providing a sample possibly containing HAdV DNA,
- Providing at least one primer pair that can specifically bind to the DNA of at least 25 different HAdV serotypes,
- Mixing the at least one primer pair with the sample,
- Establishing conditions that allow one of the primers to specifically bind to one of the DNA strands of every single one of said at least 25 HAdV serotypes,
- Amplifying regions of the DNA of each of said at least 25 HAdV serotypes actually present in the sample, wherein said regions of the DNA are flanked by the at least one primer pair,
- Detecting amplified DNA regions, quantitatively and/or under real-time conditions.

32. (New) A method for the detection of HAdV DNA in a sample, comprising the following steps:

- Providing a sample possibly containing HAdV DNA,
- Providing at least one primer pair that can specifically bind to the DNA of at least 15 different HAdV serotypes,
- Providing a probe that can specifically bind – in the region flanked by at least one said primer pair – to the DNA of said at least 15 different HAdV serotypes,

- Mixing the at least one primer pair with the sample,
- Mixing the probe with the sample,
- Establishing conditions that allow one of the primers to anneal to one of the DNA strands of every single one of said at least 15 HAdV types,
- Amplifying the regions of the DNA of all of said at least 15 HAdV serotypes actually present in the sample, wherein said regions of the DNA are flanked by the at least one primer pair,
- Establishing conditions that allow the probe to specifically bind to sections of the amplified regions,
- Detecting amplified DNA regions to which a probe has bound, quantitatively and/or under real-time conditions.

33. (New) The method according to one of claims 30, 31 or 32, wherein the amplification uses a primer that comprises at least one of the following:

a) the sequence SEQ ID NO. 1,

b) a sequence with a homology greater than 78% with respect to SEQ ID NO. 1, or

c) a sequence that is complementary to at least one of the nucleic acids according to a) or b).

34. (New) The method according to claim 33, wherein the amplification further uses a primer that comprises at least one of the following:

a) the sequence SEQ ID NO. 2,

b) a sequence with a homology greater than 78 % with respect to SEQ ID NO. 2, or

c) a sequence that is complementary to at least one of the nucleic acids according to a) or b).

35. (New) The method according to one of claims 30, 32, 33 or 34, wherein said probe comprises a nucleic acid comprising at least one of the following:

a) the sequence SEQ ID NO. 3,

b) a sequence with homology greater than 78% with respect to SEQ ID NO. 3, or

c) a sequence that is complementary to at least one of the nucleic acids according to a) or b).

36. (New) The method according to one of claims 30, 31, 32, 33, 34 or 35, wherein a TaqMan PCR process is used for amplification and detection.

37. (New) A kit, comprising one primer pair, said primer pair consisting of two primers, wherein said two primers comprise at least one of the following:

a) the sequence SEQ ID NO. 1 and SEQ ID NO. 2, respectively

b) a sequence with homology of greater than 78% with respect to SEQ ID NO. 1 and SEQ ID NO. 2, respectively, or

c) a sequence that is complementary to at least one of the nucleic acids according to a) or b), and further comprising one probe, said probe comprising at least one of the following:

d) the sequence SEQ ID NO. 3,

e) a sequence with homology greater than 78% with respect to SEQ ID NO. 3, or

f) a sequence that is complementary to at least one nucleic acid according to d) or e).

38. (New) A method to characterize HAdV serotypes, comprising the following steps:

- Detecting HAdV DNA in a sample in accordance with one of claims 30, 31, 32, 33, 34, 35, or 36, and

- Characterizing detected HAdV DNA that is present in the sample.